

WHAT IS CLAIMED IS:

1. An isolated or recombinant nucleic acid, comprising a polynucleotide sequence selected from the group consisting of:

5 (a) a polynucleotide sequence comprising the mature polypeptide coding region of a sequence selected from SEQ ID NO:1 to SEQ ID NO:7, or a complementary polynucleotide sequence thereof;

10 (b) a polynucleotide sequence encoding a polypeptide, the polypeptide comprising an amino acid sequence having at least 90% amino acid sequence identity to the mature polypeptide region of a sequence selected from SEQ ID NO:8 to SEQ ID NO:14, or a complementary polynucleotide sequence thereof;

(c) a polynucleotide sequence which hybridizes under highly stringent conditions over substantially the entire length of polynucleotide sequence (a) or (b);

15 (d) a polynucleotide sequence comprising a fragment of (a), (b), or (c), which fragment encodes a polypeptide having T-cell proliferative activity in the presence of a p35 polypeptide.

2. The nucleic acid of claim 1, wherein the nucleic acid encodes a polypeptide having T-cell proliferative activity in the presence of a p35 polypeptide, the p35 polypeptide comprising a sequence selected from a mature polypeptide region of a wild-type p35 polypeptide and a mature polypeptide region of a modified p35 polypeptide.

20 3. The nucleic acid of claim 2, wherein the p35 polypeptide comprises a sequence comprising amino acid residues 23 to 219 of SEQ ID NO:36.

4. The nucleic acid of claim 3, wherein the p35 polypeptide comprises a sequence comprising amino acid residues 23 to 219 of SEQ ID NO:31 or SEQ ID NO:32.

25 5. An isolated or recombinant nucleic acid, comprising a polynucleotide sequence encoding a modified p40 polypeptide comprising a modification at an equivalent position to that in the amino acid sequence of a human p40 polypeptide (SEQ ID NO:15), the modification selected from the group consisting of:

(a) a substitution of the specified amino acid for a different amino acid at one or more equivalent position selected from Leu62, Ser71, Gln78, His99, Thr127, Arg130, Lys185, Glu186, Tyr187, Glu188, Ser190, Asp196, Met211, Val289, Ser305, Ser307, Arg309, and Gln311;

(b) a deletion of equivalent amino acid residues Arg181 to Asn184 inclusive, or a substitution, of equivalent amino acid residues Arg181 to Asn184 inclusive, for the amino acids Ser-(Leu or Met)-(Glu or Asp)-His-Arg;

(c) a deletion of equivalent amino acid residues Asp287 and Arg288; and

(d) at least two of (a), (b), or (c);

wherein the numbering of amino acid residue positions corresponds to that of SEQ ID NO:15.

6. The nucleic acid of claim 5, wherein the modified p40 polypeptide is a modification of a p40 polypeptide selected from the group consisting of p40 polypeptides encoded by nucleic acids having the GenBank accession numbers: M65272, M65290, U19841, U19834, Y11129, U83184, Y07762, AF054607, U49100, AF091134, U57752, U10160, AF007576, AF004024, U11815, U08317, X97019, AF082494, AF133197, U16674, M86671, S82426, AF097507, and AF046211.

7. The nucleic acid of claim 5, wherein the modified p40 polypeptide is a modification of a human p40 polypeptide comprising amino acid residues 23 to 328 of SEQ ID NO:15.

8. The nucleic acid of claim 5, wherein the modified p40 polypeptide comprises one or more substitution selected from the group consisting of:

Leu62Ser; Ser71Thr; Gln78His; His99(Arg or Gln); Thr127(Ser or Ile); Arg130Lys; Lys185Glu; Glu186Tyr; Tyr187(Lys or Asn); Glu188Lys; Ser190(Arg or Thr); Asp196Gly; Met211Val; Val289(Ile or Leu); Ser305Lys; Ser307Arg; Arg309Gln; and Gln311Arg.

9. The nucleic acid of claim 5, wherein the encoded polypeptide comprises one or more substitution selected from the group consisting of:

Lys27Glu; Asp29Asn; Asp40Asn; Met45Thr; Thr49Ala; Glu67Gly, His91Arg;  
Glu95(Ala or Thr), Val96Ala; Glu122Lys; Asn125Ala; Asn135Asp; Arg139His; Thr147Ala;  
Thr153Lys; Ser155Thr; Ser163Thr; Gln166(Arg or His), Ala172Thr; Ala173Val;  
Thr174Leu; Ala177Glu; Glu178Asp; Arg179Leu; Val180Gly; Ala201Ser; Val212Leu;  
5 Asp213Glu; Val215Ile; Ser226Arg; Lys244Arg; Gln251His; Val254Ile; Ser255Asn;  
Glu257Gly; Thr264(Ala or Ile); Thr272Met; Cys274Gly; Val275Ile; Lys280Arg; Ser281Asn;  
Lys285Asp; Lys286Arg; Phe290Ser; Thr291(Met or Val); Lys293Gln; Thr297Lys;  
Ile299(Thr or Val); Arg301His; Asn303Asp; Ser318Phe; Glu321Asp; Pro326Ser;  
Cys327Leu; and Ser328(Gly or Gln) .

10                    10. The nucleic acid of claim 5, wherein the encoded polypeptide has T-cell  
proliferative activity in the presence of a p35 polypeptide.

11. An isolated or recombinant nucleic acid, comprising:

a polynucleotide sequence encoding a polypeptide, the polypeptide comprising a  
sequence having at least about 90% amino acid sequence identity to the amino acid sequence  
15 IWEL-X<sub>27</sub>-K-X<sub>29</sub>-VYVVELDWYP-X<sub>40</sub>-APGE-X<sub>45</sub>-VVL-X<sub>49</sub>-CDTPEEDGITWT-X<sub>62</sub>-  
DQSS-X<sub>67</sub>-VLG-X<sub>71</sub>-GKTLTI-X<sub>78</sub>-VKEFGDAGQYTC-X<sub>91</sub>-KGG-X<sub>95</sub>-X<sub>96</sub>-LS-X<sub>99</sub>-  
SLLLLHKKEDGIWSTDILKDQK-X<sub>122</sub>-PK-X<sub>125</sub>-K-X<sub>127</sub>-FL-X<sub>130</sub>-CEAK-X<sub>135</sub>-YSG-X<sub>139</sub>-  
FTCWWLT-X<sub>147</sub>-ISTDL-X<sub>153</sub>-F-X<sub>155</sub>-VKSSRGS-X<sub>163</sub>-DP-X<sub>166</sub>-GVTCG-X<sub>172</sub>-X<sub>173</sub>-X<sub>174</sub>-LS-  
X<sub>177</sub>-X<sub>178</sub>-X<sub>179</sub>-X<sub>180</sub>-X<sub>181</sub>-X<sub>182</sub>-X<sub>183</sub>-X<sub>184</sub>-X<sub>185</sub>-X<sub>186</sub>-X<sub>187</sub>-X<sub>188</sub>-Y-X<sub>190</sub>-VECQE-X<sub>196</sub>-SACP-  
20 X<sub>201</sub>-AEESLPIEV-X<sub>211</sub>-X<sub>212</sub>-X<sub>213</sub>-A-X<sub>215</sub>-HKLKYENYTS-X<sub>226</sub>-FFIRDIKPDPPKNLQL-  
X<sub>244</sub>-PLKNSR-X<sub>251</sub>-VE-X<sub>254</sub>-X<sub>255</sub>-W-X<sub>257</sub>-YPDTWS-X<sub>264</sub>-PHSYFSLTF-X<sub>274</sub>-X<sub>275</sub>-QVQG-  
X<sub>280</sub>-X<sub>281</sub>-KRE-X<sub>285</sub>-X<sub>286</sub>-X<sub>287</sub>-X<sub>288</sub>-X<sub>289</sub>-F-X<sub>291</sub>-D-X<sub>293</sub>-TSA-X<sub>297</sub>-V-X<sub>299</sub>-C-X<sub>301</sub>-K-X<sub>303</sub>-A-  
X<sub>305</sub>-I-X<sub>307</sub>-V-X<sub>309</sub>-A-X<sub>311</sub>-DRY-X<sub>315</sub>-SS-X<sub>318</sub>-WS-X<sub>321</sub>-WASV-X<sub>326</sub>-X<sub>327</sub>-X<sub>328</sub>, or a  
conservatively substituted variation thereof,

25                    where X<sub>27</sub> is K or E; X<sub>29</sub> is D or N; X<sub>40</sub> is D or N; X<sub>45</sub> is M or T; X<sub>49</sub> is T or A; X<sub>62</sub> is  
S; X<sub>67</sub> is E or G; X<sub>71</sub> is T; X<sub>78</sub> is H; X<sub>91</sub> is H or R; X<sub>95</sub> is E, A, K, or T; X<sub>96</sub> is V or A; X<sub>99</sub> is R  
or Q; X<sub>122</sub> is E or K; X<sub>125</sub> is N or A; X<sub>127</sub> is S or I; X<sub>130</sub> is K; X<sub>135</sub> is N or D; X<sub>139</sub> is R or H;  
X<sub>147</sub> is T or A; X<sub>153</sub> is T or K; X<sub>155</sub> is S or T; X<sub>163</sub> is S or T; X<sub>166</sub> is Q, R, or H; X<sub>172</sub> is A or T;  
X<sub>173</sub> is A or V; X<sub>174</sub> is T or L; X<sub>177</sub> is A or E; X<sub>178</sub> is E or D; X<sub>179</sub> is R, L, or K; X<sub>180</sub> is V or G;  
30 X<sub>181</sub> to X<sub>184</sub> inclusive is deleted, or is replaced with the sequence S-(L or M)-(E or D)-H-R;

X<sub>185</sub> is E; X<sub>186</sub> is Y; X<sub>187</sub> is K or N; X<sub>188</sub> is K; X<sub>190</sub> is R or T; X<sub>196</sub> is G; X<sub>201</sub> is A or S; X<sub>211</sub> is V; X<sub>212</sub> is V or L; X<sub>213</sub> is D or E; X<sub>215</sub> is V or I; X<sub>226</sub> is S or R; X<sub>244</sub> is K or R; X<sub>251</sub> is Q or H; X<sub>254</sub> is V or I; X<sub>255</sub> is S or N; X<sub>257</sub> is E or G; X<sub>264</sub> is T or A; X<sub>274</sub> is C or G; X<sub>275</sub> is V or I; X<sub>280</sub> is K or R; X<sub>281</sub> is S or N; X<sub>285</sub> is K or D; X<sub>286</sub> is K or R; X<sub>287</sub> is D or is deleted; X<sub>288</sub> is R or is deleted; X<sub>289</sub> is I or L; X<sub>291</sub> is T or M; X<sub>293</sub> is K or Q; X<sub>297</sub> is T or K; X<sub>299</sub> is I, T, or V; X<sub>301</sub> is R or H; X<sub>303</sub> is N or D; X<sub>305</sub> is K; X<sub>307</sub> is R; X<sub>309</sub> is Q; X<sub>311</sub> is R; X<sub>315</sub> is Y or H; X<sub>318</sub> is S or F; X<sub>321</sub> is E or D; X<sub>326</sub> is P or S; X<sub>327</sub> is C or L; and X<sub>328</sub> is S, G, or Q.

12. The nucleic acid of claim 11, wherein the encoded polypeptide comprises at its N-terminus a sequence having at least about 90% amino acid sequence identity to the amino acid sequence M-X<sub>2</sub>-X<sub>3</sub>-QQLV-X<sub>8</sub>-SWFSLV-X<sub>15</sub>-LASPL-X<sub>21</sub>-A, or a conservatively substituted variation thereof,

where X<sub>2</sub> is C or H; X<sub>3</sub> is H or P; X<sub>8</sub> is I or V; X<sub>15</sub> is F or L; and X<sub>21</sub> is V or M.

13. The nucleic acid of claim 11, wherein the encoded polypeptide has T-cell proliferative activity in the presence of a p35 polypeptide

14. The nucleic acid of claim 11, wherein the encoded polypeptide comprises an amino acid sequence selected from the group consisting of the mature polypeptide region of SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:14.

15. The nucleic acid of claim 11, wherein the encoded polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:14.

16. The nucleic acid of claim 11, comprising a polynucleotide sequence selected from the group consisting of the mature polypeptide coding region of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, and SEQ ID NO:7.

17. The nucleic acid of claim 16, comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, and SEQ ID NO:7.

18. An isolated or recombinant nucleic acid comprising a polynucleotide  
5 sequence encoding a polypeptide, the encoded polypeptide comprising:  
an amino acid sequence comprising at least 10 contiguous amino acid residues of any one of SEQ ID NOS:8-14, and

one or more amino acid substitution at an equivalent position to that of the amino acid sequence of a p40 polypeptide identified by SEQ ID NO:15, the one or more substitution  
10 selected from: Leu62Ser; Ser71Thr; Gln78His; His99(Arg or Gln); Thr127(Ser or Ile); Arg130Lys; Lys185Glu; Glu186Tyr; Tyr187(Lys or Asn); Glu188Lys; Ser190(Arg or Thr); Asp196Gly; Met211Val; Val289(Ile or Leu); Ser305Lys; Ser307Arg; Arg309Gln; and Gln311Arg; wherein the numbering of the amino acid residues corresponds to that of SEQ ID NO:15.

19. The nucleic acid of claim 18, wherein the encoded polypeptide has T-cell proliferative activity in the presence of a p35 polypeptide.

20. The nucleic acid of claim 18, wherein the encoded polypeptide comprises at least 50 contiguous amino acid residues of any one of SEQ ID NOS:8-14.

21. The nucleic acid of claim 18, wherein the encoded polypeptide  
20 comprises at least 200 contiguous amino acid residues of any one of SEQ ID NOS:8-14.

22. The nucleic acid of claim 18, wherein the encoded polypeptide comprises at least 270 contiguous amino acid residues of any one of SEQ ID NOS:8-14.

23. The nucleic acid of claim 18, wherein the encoded polypeptide comprises at least 285 contiguous amino acid residues of any one of SEQ ID NOS:8-14.

24. An isolated or recombinant nucleic acid comprising a polynucleotide  
25 sequence encoding a polypeptide, the encoded polypeptide comprising at least 270 contiguous amino acid residues of a sequence of a mature polypeptide region selected from

the group consisting of: amino acid residues 23-324 of SEQ ID NO:8; amino acid residues 23-327 of SEQ ID NO:9, amino acid residues 23-327 of SEQ ID NO:10, amino acid residues 23-327 of SEQ ID NO:11, amino acid residues 23-322 of SEQ ID NO:12, amino acid residues 23-324 of SEQ ID NO:13, and amino acid residues 23-329 of SEQ ID NO:14.

5                    **25.** The nucleic acid of claim **24**, comprising a polynucleotide sequence selected from the group consisting of: nucleotides 67 to 972 of SEQ ID NO:1; nucleotides 67 to 981 of SEQ ID NO:2; nucleotides 67 to 981 of SEQ ID NO:3; nucleotides 67 to 981 of SEQ ID NO:4, nucleotides 67 to 966 of SEQ ID NO:5; nucleotides 67 to 972 of SEQ ID NO:6; and nucleotides 67 to 987 of SEQ ID NO:7.

10                    **26.** A cell comprising the nucleic acid of claim **1, 5, 11, 18, or 24.**

**27.** The cell of claim **26**, wherein the cell expresses a polypeptide encoded by the nucleic acid.

**28.** A vector comprising the nucleic acid of claim **1, 5, 11, 18, or 24.**

15                    **29.** The vector of claim **28**, wherein the vector comprises a plasmid, a cosmid, a phage, or a virus.

**30.** The vector of claim **28**, wherein the vector is an expression vector.

**31.** A cell transduced by the vector of claim **28.**

**32.** A composition comprising the nucleic acid of claim **1, 5, 11, 18, or 24** and an excipient.

20                    **33.** The composition of claim **32**, wherein the excipient is a pharmaceutically acceptable excipient.

**34.** A composition produced by digesting one or more nucleic acids of claim **1, 5, 11, 18, or 24** with a restriction endonuclease, an RNase, or a DNase.

35. A composition produced by a process comprising incubating one or more nucleic acids of claim 1, 5, 11, 18, or 24 in the presence of deoxyribonucleotide triphosphates and a nucleic acid polymerase.

36. The composition of claim 35, wherein the nucleic acid polymerase is a  
5 thermostable polymerase.

37. An isolated or recombinant polypeptide encoded by the nucleic acid of  
claim 1, 5, 11, 18, or 24.

38. The polypeptide of claim 37, comprising a sequence selected from the group consisting of: amino acid residues 23-324 of SEQ ID NO:8; amino acid residues 23-  
10 327 of SEQ ID NO:9, amino acid residues 23-327 of SEQ ID NO:10, amino acid residues 23-327 of SEQ ID NO:11, amino acid residues 23-322 of SEQ ID NO:12, amino acid residues 23-324 of SEQ ID NO:13, and amino acid residues 23-329 of SEQ ID NO:14.

39. The polypeptide of claim 38, comprising an N-terminal sequence corresponding to amino acid residues 1-22 of a sequence selected from: SEQ ID NO:8, SEQ  
15 ID NO:9, SEQ ID NO:11, and SEQ ID NO:13.

40. The polypeptide of claim 37, having T-cell proliferative activity in the presence of a p35 polypeptide.

41. An isolated or recombinant modified p40 polypeptide comprising a modification at an equivalent position to that in the amino acid sequence of a human p40  
20 polypeptide (SEQ ID NO:15), the modification selected from the group consisting of:

(a) a substitution of the specified amino acid for a different amino acid at one or more equivalent position selected from Leu62, Ser71, Gln78, His99, Thr127, Arg130, Lys185, Glu186, Tyr187, Glu188, Ser190, Asp196, Met211, Val289, Ser305, Ser307, Arg309, and Gln311;

25 (b) a deletion of equivalent amino acid residues Arg181 to Asn184 inclusive, or a substitution of equivalent amino acid residues Arg181 to Asn184 inclusive for the amino acid residues Ser-(Leu or Met)-(Glu or Asp)-His-Arg;

(c) a deletion of equivalent amino acid residues Asp287 and Arg288; and

(d) at least two of (a), (b), or (c);  
wherein the numbering of amino acid residue positions corresponds to that of SEQ ID  
NO:15.

42. The polypeptide of claim 41, comprising one or more substitution  
5 selected from the group consisting of:

Leu62Ser; Ser71Thr; Gln78His; His99(Arg or Gln); Thr127(Ser or Ile);  
Arg130Lys; Lys185Glu; Glu186Tyr; Tyr187(Lys or Asn); Glu188Lys; Ser190(Arg or Thr);  
Asp196Gly; Met211Val; Val289(Ile or Leu); Ser305Lys; Ser307Arg; Arg309Gln; and  
Gln311Arg.

10 43. The polypeptide of claim 41, comprising one or more substitution  
selected from the group consisting of:

Lys27Glu; Asp29Asn; Asp40Asn; Met45Thr; Thr49Ala; Glu67Gly; His91Arg;  
Glu95(Ala or Thr); Val96Ala; Glu122Lys; Asn125Ala; Asn135Asp; Arg139His; Thr147Ala;  
Thr153Lys; Ser155Thr; Ser163Thr; Gln166(Arg or His); Ala172Thr; Ala173Val;  
15 Thr174Leu; Ala177Glu; Glu178Asp; Arg179Leu; Val180Gly; Ala201Ser; Val212Leu;  
Asp213Glu; Val215Ile; Ser226Arg; Lys244Arg; Gln251His; Val254Ile; Ser255Asn;  
Glu257Gly; Thr264(Ala or Ile); Thr272Met; Cys274Gly; Val275Ile; Lys280Arg; Ser281Asn;  
Lys285Asp; Lys286Arg; Phe290Ser; Thr291(Met or Val); Lys293Gln; Thr297Lys;  
Ile299(Thr or Val); Arg301His; Asn303Asp; Ser318Phe; Glu321Asp; Pro326Ser;  
20 Cys327Leu; and Ser328(Gly or Gln).

44. The polypeptide of claim 41, having T-cell proliferative activity in the  
presence of a p35 polypeptide.

45. An isolated or recombinant polypeptide, the polypeptide comprising a  
sequence having at least about 90% amino acid sequence identity to the amino acid sequence  
25 IWEL-X<sub>27</sub>-K-X<sub>29</sub>-VYVVELDWYP-X<sub>40</sub>-APGE-X<sub>45</sub>-VVL-X<sub>49</sub>-CDTPEEDGITWT-X<sub>62</sub>-  
DQSS-X<sub>67</sub>-VLG-X<sub>71</sub>-GKTLTI-X<sub>78</sub>-VKEFGDAGQYTC-X<sub>91</sub>-KGG-X<sub>95</sub>-X<sub>96</sub>-LS-X<sub>99</sub>-  
SLLLLHKKEDGIWSTDILKDQK-X<sub>122</sub>-PK-X<sub>125</sub>-K-X<sub>127</sub>-FL-X<sub>130</sub>-CEAK-X<sub>135</sub>-YSG-X<sub>139</sub>-  
FTCWWLT-X<sub>147</sub>-ISTDL-X<sub>153</sub>-F-X<sub>155</sub>-VKSSRGs-X<sub>163</sub>-DP-X<sub>166</sub>-GVTCG-X<sub>172</sub>-X<sub>173</sub>-X<sub>174</sub>-LS-  
X<sub>177</sub>-X<sub>178</sub>-X<sub>179</sub>-X<sub>180</sub>-X<sub>181</sub>-X<sub>182</sub>-X<sub>183</sub>-X<sub>184</sub>-X<sub>185</sub>-X<sub>186</sub>-X<sub>187</sub>-X<sub>188</sub>-Y-X<sub>190</sub>-VECQE-X<sub>196</sub>-SACP-



X<sub>201</sub>-AEESLPIEV-X<sub>211</sub>-X<sub>212</sub>-X<sub>213</sub>-A-X<sub>215</sub>-HKLKYENYTS-X<sub>226</sub>-FFIRDIKPDPPKNLQL-  
X<sub>244</sub>-PLKNSR-X<sub>251</sub>-VE-X<sub>254</sub>-X<sub>255</sub>-W-X<sub>257</sub>-YPTDWS-X<sub>264</sub>-PHSYFSLTF-X<sub>274</sub>-X<sub>275</sub>-QVQG-  
X<sub>280</sub>-X<sub>281</sub>-KRE-X<sub>285</sub>-X<sub>286</sub>-X<sub>287</sub>-X<sub>288</sub>-X<sub>289</sub>-F-X<sub>291</sub>-D-X<sub>293</sub>-TSA-X<sub>297</sub>-V-X<sub>299</sub>-C-X<sub>301</sub>-K-X<sub>303</sub>-A-  
X<sub>305</sub>-I-X<sub>307</sub>-V-X<sub>309</sub>-A-X<sub>311</sub>-DRY-X<sub>315</sub>-SS-X<sub>318</sub>-WS-X<sub>321</sub>-WASV-X<sub>326</sub>-X<sub>327</sub>-X<sub>328</sub>, or a

5 conservatively substituted variation thereof,

where X<sub>27</sub> is K or E; X<sub>29</sub> is D or N; X<sub>40</sub> is D or N; X<sub>45</sub> is M or T; X<sub>49</sub> is T or A; X<sub>62</sub> is  
S; X<sub>67</sub> is E or G; X<sub>71</sub> is T; X<sub>78</sub> is H; X<sub>91</sub> is H or R; X<sub>95</sub> is E, A, K, or T; X<sub>96</sub> is V or A; X<sub>99</sub> is R  
or Q; X<sub>122</sub> is E or K; X<sub>125</sub> is N or A; X<sub>127</sub> is S or I; X<sub>130</sub> is K; X<sub>135</sub> is N or D; X<sub>139</sub> is R or H;  
X<sub>147</sub> is T or A; X<sub>153</sub> is T or K; X<sub>155</sub> is S or T; X<sub>163</sub> is S or T; X<sub>166</sub> is Q, R, or H; X<sub>172</sub> is A or T;  
10 X<sub>173</sub> is A or V; X<sub>174</sub> is T or L; X<sub>177</sub> is A or E; X<sub>178</sub> is E or D; X<sub>179</sub> is R, L, or K; X<sub>180</sub> is V or G;  
X<sub>181</sub> to X<sub>184</sub> inclusive is deleted, or is replaced with the sequence S-(L or M)-(E or D)-H-R;  
X<sub>185</sub> is E; X<sub>186</sub> is Y; X<sub>187</sub> is K or N; X<sub>188</sub> is K; X<sub>190</sub> is R or T; X<sub>196</sub> is G; X<sub>201</sub> is A or S; X<sub>211</sub> is  
V; X<sub>212</sub> is V or L; X<sub>213</sub> is D or E; X<sub>215</sub> is V or I; X<sub>226</sub> is S or R; X<sub>244</sub> is K or R; X<sub>251</sub> is Q or H;  
X<sub>254</sub> is V or I; X<sub>255</sub> is S or N; X<sub>257</sub> is E or G; X<sub>264</sub> is T or A; X<sub>274</sub> is C or G; X<sub>275</sub> is V or I; X<sub>280</sub>  
15 is K or R; X<sub>281</sub> is S or N; X<sub>285</sub> is K or D; X<sub>286</sub> is K or R; X<sub>287</sub> is D or is deleted; X<sub>288</sub> is R or is  
deleted; X<sub>289</sub> is I or L; X<sub>291</sub> is T or M; X<sub>293</sub> is K or Q; X<sub>297</sub> is T or K; X<sub>299</sub> is I, T, or V; X<sub>301</sub> is  
R or H; X<sub>303</sub> is N or D; X<sub>305</sub> is K; X<sub>307</sub> is R; X<sub>309</sub> is Q; X<sub>311</sub> is R; X<sub>315</sub> is Y or H; X<sub>318</sub> is S or F;  
X<sub>321</sub> is E or D; X<sub>326</sub> is P or S; X<sub>327</sub> is C or L; and X<sub>328</sub> is S, G, or Q.

46. The polypeptide of claim 45, having T-cell proliferative activity in the  
20 presence of a p35 polypeptide.

47. The polypeptide of claim 45, comprising a sequence selected from the  
group consisting of: amino acid residues 23-324 of SEQ ID NO:8; amino acid residues 23-  
327 of SEQ ID NO:9, amino acid residues 23-327 of SEQ ID NO:10, amino acid residues  
23-327 of SEQ ID NO:11, amino acid residues 23-322 of SEQ ID NO:12, amino acid  
25 residues 23-324 of SEQ ID NO:13, and amino acid residues 23-329 of SEQ ID NO:14.

48. A polypeptide comprising at least 100 contiguous amino acid residues of  
a protein encoded by a coding polynucleotide sequence, the polynucleotide sequence selected  
from the group consisting of:

(a) nucleotides 67 to 972 of SEQ ID NO:1; nucleotides 67 to 981 of SEQ ID NO:2; nucleotides 67 to 981 of SEQ ID NO:3; nucleotides 67 to 981 of SEQ ID NO:4, nucleotides 67 to 966 of SEQ ID NO:5; nucleotides 67 to 972 of SEQ ID NO:6; and nucleotides 67 to 987 of SEQ ID NO:7;

(b) a coding polynucleotide sequence that encodes a first polypeptide selected from amino acid residues 23-324 of SEQ ID NO:8; amino acid residues 23-327 of SEQ ID NO:9, amino acid residues 23-327 of SEQ ID NO:10, amino acid residues 23-327 of SEQ ID NO:11, amino acid residues 23-322 of SEQ ID NO:12, amino acid residues 23-324 of SEQ ID NO:13, and amino acid residues 23-329 of SEQ ID NO:14; and

(c) a complementary polynucleotide sequence which hybridizes under highly stringent conditions over substantially an entire length of a polynucleotide sequence of (a) or (b).

49. The polypeptide of claim 48, comprising at least 200 contiguous amino acid residues of the encoded protein.

50. The polypeptide of claim 48, comprising a sequence selected from the group consisting of the mature polypeptide region of SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:14.

51. The polypeptide of claim 48, comprising a sequence selected from the group consisting of SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:14.

52. The polypeptide of claim 48, having T-cell proliferative activity in the presence of a p35 polypeptide.

53. The polypeptide of claim 41, 45, or 48, comprising a secretion/localization sequence or a polypeptide subsequence that facilitates purification.

54. The polypeptide of claim 53, wherein the subsequence that facilitates purification is selected from the group consisting of: an epitope tag, a polyhistidine tag, and a GST fusion.

55. The polypeptide of claim 41, 45, or 48, comprising a Met at the N-terminus.

56. The polypeptide of claim 41, 45, or 48, comprising a modified amino acid.

5 57. The polypeptide of claim 56, wherein the modified amino acid is selected from the group consisting of: a glycosylated amino acid, a PEGylated amino acid, a farnesylated amino acid, an acetylated amino acid, and a biotinylated amino acid.

58. A composition comprising the polypeptide of claim 41, 45, or 48.

59. The composition of claim 58, further comprising a p35 polypeptide.

10 60. The composition of claim 58, further comprising an excipient.

61. The composition of claim 60, wherein the excipient is a pharmaceutically acceptable excipient.

62. A polypeptide which is specifically bound by a polyclonal antisera raised against at least one antigen, said at least one antigen comprising at least one amino acid sequence of SEQ ID NO:8 to SEQ ID NO:14, or a fragment thereof, wherein the antisera is subtracted with a p40 polypeptide encoded by a nucleic acid corresponding to one or more of GenBank accession number: M65272, M65290, U19841, U19834, Y11129, U83184, Y07762, AF054607, U49100, AF091134, U57752, U10160, AF007576, AF004024, U11815, U08317, X97019, AF082494, AF133197, U16674, M86671, S82426, AF097507, and  
15  
20 AF046211.

63. An antibody or antisera produced by administering the polypeptide of claim 37, 41, 45, or 48 to a mammal, which antibody specifically binds at least one antigen, said at least one antigen comprising a polypeptide comprising one or more of the amino acid sequences of SEQ ID NO:8 to SEQ ID NO:14, or a fragment thereof, which antibody or  
25 antisera does not specifically bind to a p40 polypeptide encoded by a nucleic acid corresponding to one or more of GenBank accession number: M65272, M65290, U19841, U19834, Y11129, U83184, Y07762, AF054607, U49100, AF091134, U57752, U10160,

AF007576, AF004024, U11815, U08317, X97019, AF082494, AF133197, U16674, M86671, S82426, AF097507, and AF046211.

5           **64.** An antibody or antisera which specifically binds a polypeptide, the polypeptide comprising a sequence selected from the group consisting of SEQ ID NO:8 to SEQ ID NO:14, wherein the antibody does not specifically bind to a p40 polypeptide encoded by a nucleic acid corresponding to one or more of GenBank accession number: M65272, M65290, U19841, U19834, Y11129, U83184, Y07762, AF054607, U49100, AF091134, U57752, U10160, AF007576, AF004024, U11815, U08317, X97019, AF082494, AF133197, U16674, M86671, S82426, AF097507, and AF046211.

10           **65.** A method of producing a polypeptide, the method comprising:  
          introducing into a population of cells a nucleic acid of claim 1, 5, 11, 18, or 24, the nucleic acid operatively linked to a regulatory sequence effective to produce the encoded polypeptide; and  
          culturing the cells in a culture medium to produce the polypeptide.

15           **66.** A method of producing a polypeptide, the method comprising  
          introducing into a population of cells a recombinant expression vector comprising the nucleic acid of claim 1, 5, 11, 18, or 24; and  
          culturing the cells in a culture medium under conditions suitable to produce the polypeptide encoded by the expression vector.

20           **67.** A method of inducing proliferation of T-lymphocytes, the method comprising: contacting the T-lymphocytes with a composition of claim 58, thereby inducing proliferation of the T-lymphocytes.

**68.** The method of claim 67, ~~wherein~~ the T-lymphocytes are in culture.

25           **69.** A method of inducing production of IFN- $\gamma$  in T-lymphocytes, the method comprising:  
          contacting the T-lymphocytes with a composition of claim 58, thereby inducing production of IFN- $\gamma$  in the T-lymphocytes.

70. The method of claim 69, wherein the T-lymphocytes are in culture.

71. A method for making a modified or recombinant nucleic acid, the method comprising: recursively recombining one or more nucleic acid of claim 1, 5, 11, 18, or 24 with one or more additional nucleic acid, the additional nucleic acid encoding a p40 polypeptide or subsequence thereof.

72. The method of claim 71, wherein said recursive recombination produces at least one library of recombinant modified p40 nucleic acids.

73. A nucleic acid library produced by the method of claim 72.

74. A population of cells comprising the library of claim 73.

75. A recombinant modified p40 nucleic acid produced by the method of claim 72.

76. A cell comprising the nucleic acid of claim 75.

77. The method of claim 71, wherein the recursive recombination is performed *in vitro*.

78. The method of claim 71, wherein the recursive recombination is performed *in vivo* or *ex vivo*.

79. A composition comprising two or more nucleic acids of claim 1, 5, 11, 18, or 24.

80. The composition of claim 79, wherein the composition comprises a library comprising at least ten nucleic acids.

81. A method of producing a modified p40 nucleic acid comprising mutating a nucleic acid of claim 1, 5, 11, 18, or 24.

82. The modified p40 nucleic acid produced by the method of claim 81.

83. A nucleic acid which comprises a unique subsequence in a nucleic acid selected from SEQ ID NO:1 to SEQ ID NO:7, wherein the unique subsequence is unique as compared to a nucleic acid sequence of a known p40 nucleic acid sequence or a nucleic acid corresponding to any of GenBank accession number: M65272, M65290, U19841, U19834,  
5 Y11129, U83184, Y07762, AF054607, U49100, AF091134, U57752, U10160, AF007576, AF004024, U11815, U08317, X97019, AF082494, AF133197, U16674, M86671, S82426 , AF097507, and AF046211.

84. A polypeptide which comprises a unique subsequence in a polypeptide selected from: SEQ ID NO:8 to SEQ ID NO:14, wherein the unique subsequence is unique as  
10 compared to a sequence of a known p40 polypeptide or a sequence of a polypeptide encoded by a nucleic acid corresponding to any of GenBank accession number: M65272, M65290, U19841, U19834, Y11129, U83184, Y07762, AF054607, U49100, AF091134, U57752, U10160, AF007576, AF004024, U11815, U08317, X97019, AF082494, AF133197, U16674, M86671, S82426 , AF097507, and AF046211.

85. A target nucleic acid which hybridizes under stringent conditions to a unique coding oligonucleotide which encodes a unique subsequence in a polypeptide selected from: SEQ ID NO:8 to SEQ ID NO:14, wherein the unique subsequence is unique as  
15 compared to a sequence of a known p40 polypeptide or a sequence of a polypeptide encoded by a nucleic acid corresponding to any of GenBank accession number: M65272, M65290, U19841, U19834, Y11129, U83184, Y07762, AF054607, U49100, AF091134, U57752,  
20 U10160, AF007576, AF004024, U11815, U08317, X97019, AF082494, AF133197, U16674, M86671, S82426 , AF097507, and AF046211.

86. The nucleic acid of claim 85, wherein the stringent conditions are selected such that a perfectly complementary oligonucleotide to the unique coding  
25 oligonucleotide hybridizes to the unique coding oligonucleotide with at least a 5x higher signal to noise ratio than for hybridization of the perfectly complementary oligonucleotide to a control nucleic acid corresponding to any of GenBank accession number: M65272, M65290, U19841, U19834, Y11129, U83184, Y07762, AF054607, U49100, AF091134, U57752, U10160, AF007576, AF004024, U11815, U08317, X97019, AF082494, AF133197,

U16674, M86671, S82426 , AF097507, and AF046211, wherein the target nucleic acid hybridizes to the unique coding oligonucleotide with at least a 2x higher signal to noise ratio as compared to hybridization of the control nucleic acid to the coding oligonucleotide.

5       **87.** An isolated or recombinant nucleic acid, comprising a polynucleotide sequence selected from the group consisting of:

      (a) a polynucleotide sequence comprising the mature polypeptide coding region of a sequence selected from SEQ ID NO:16 to SEQ ID NO:25, or a complementary polynucleotide sequence thereof;

10       (b) a polynucleotide sequence encoding a polypeptide, the polypeptide comprising an amino acid sequence having at least 90% amino acid sequence identity to the mature polypeptide region of a sequence selected from SEQ ID NO:26 to SEQ ID NO:35, or a complementary polynucleotide sequence thereof;

      (c) a polynucleotide sequence which hybridizes under highly stringent conditions over substantially the entire length of polynucleotide sequence (a) or (b);

15       (d) a polynucleotide sequence comprising a fragment of (a), (b), or (c), which fragment encodes a polypeptide having T-cell proliferative activity in the presence of a p40 polypeptide.

20       **88.** The nucleic acid of claim 87, wherein the nucleic acid encodes a polypeptide having T-cell proliferative activity in the presence of a p40 polypeptide, wherein the p40 polypeptide comprises a sequence selected from a mature polypeptide region of a wild-type p40 polypeptide and a mature polypeptide region of a modified p40 polypeptide.

**89.** The nucleic acid of claim 88, wherein the p40 polypeptide comprises a sequence comprising amino acid residues 23 to 328 of SEQ ID NO:15.

25       **90.** The nucleic acid of claim 89, wherein the p40 polypeptide comprises a sequence comprising amino acid residues 23 to 324 of SEQ ID NO:8.

**91.** An isolated or recombinant nucleic acid, comprising a polynucleotide sequence encoding a modified p35 polypeptide comprising a modification at an equivalent

position to that in the amino acid sequence of a human p35 polypeptide (SEQ ID NO:36), the modification selected from the group consisting of:

(a) a substitution of the specified amino acid for a different amino acid at one or more equivalent position selected from Thr91, Met120, Ala121, Val212, Thr213, and Ala218;

(b) a insertion of one or more amino acid residues Phe-His-Leu between equivalent positions Leu19 and Ser20;

(c) a deletion of the amino acid at equivalent position Pro36

(d) at least two of (a), (b), or (c);

wherein the numbering of amino acid residue positions corresponds to that of SEQ ID

NO:36.

**92.** The nucleic acid of claim **91**, wherein the modified p35 polypeptide is a modification of a p35 polypeptide selected from the group consisting of those encoded by nucleic acids having the GenBank accession numbers: M65271, M65291, U19842, U19835, U83185, Y07761, AF054605, U49085, L35765, Y11130, U14416, U57751, AF173557, AF003542, X97018, AF177031, M86672, and S82419.

**93.** The nucleic acid of claim **91**, wherein the modified p35 polypeptide is a modification of a human p35 polypeptide comprising amino acid residues 23 to 219 of SEQ ID NO:36.

**94.** The nucleic acid of claim **91**, wherein the modified p35 polypeptide comprises one or more substitution selected from the group consisting of: Thr91(Ala or Ile); Met120Thr; Ala121Thr; Val212Met; Thr213Met; and Ala218Ser, wherein the numbering of amino acid residue positions corresponds to that of SEQ ID NO:36.

**95.** The nucleic acid of claim **91**, wherein the encoded polypeptide comprises one or more substitution selected from the group consisting of:

Cys2Tyr; Ala4(Leu or Pro); Ser6Gly; Val10Ile; Ala11Ser; Asp17His; Ala22Gly; Asn24Ser; Val27Thr; Ala28Thr; Pro30Ala; Asp31(Ser or Gly); Met34Arg; Phe35(Ser or Leu); Pro36(deleted); His39Asp; His40Tyr; Arg46Lys; Val48Ala; Met51Thr; Lys54Arg; Thr58Ile; Pro63Ser; Ile69Thr; Lys76Gln; Lys92Thr; Asn98Ala; Glu101Gly; Thr102Ile;



Phe104Leu; Leu124His; Ser125Gly; Val136Met; Thr140Ala; Asp148Asn; Ala161Thr;  
Val162Ala; Asp164Ala; Met167Leu; Phe172Val; Val177Ala; Ser181Pro; Pro186Leu;  
Asp210Asn; and insertion of one or more of 220Leu; 221Glu; 222Ser; and 223Ser,

wherein the numbering of amino acid residue positions corresponds to that of SEQ ID

5 NO:36.

**96.** The nucleic acid of claim 91, wherein the encoded polypeptide has T-cell proliferative activity in the presence of a p40 polypeptide.

**97.** An isolated or recombinant nucleic acid, comprising:

a polynucleotide sequence encoding a polypeptide, the polypeptide comprising a

10 sequence having at least about 90% amino acid sequence identity to the amino acid sequence  
R-X<sub>24</sub>-LP-X<sub>27</sub>-X<sub>28</sub>-T-X<sub>30</sub>-X<sub>31</sub>-PG-X<sub>34</sub>-X<sub>35</sub>-X<sub>36</sub>-CL-X<sub>39</sub>-X<sub>40</sub>-SQNLL-X<sub>46</sub>-A-X<sub>48</sub>-SN-X<sub>51</sub>-LQ-  
X<sub>54</sub>-A-X<sub>56</sub>-Q-X<sub>58</sub>-LEFY-X<sub>63</sub>-CTSEE-X<sub>69</sub>-DHEDIT-X<sub>76</sub>-DKTSTVEACLPLEL-X<sub>91</sub>-X<sub>92</sub>-  
NESCL-X<sub>98</sub>-SR-X<sub>101</sub>-X<sub>102</sub>-S-X<sub>104</sub>-ITNGSCLASRKTSFM-X<sub>120</sub>-X<sub>121</sub>-LC-X<sub>124</sub>-X<sub>125</sub>-  
SIYEDLKMYQ-X<sub>136</sub>-EFK-X<sub>140</sub>-MNAKLLM-X<sub>148</sub>-PKRQIFLDQNML-X<sub>161</sub>-X<sub>162</sub>-I-X<sub>164</sub>-EL-  
15 X<sub>167</sub>-QALN-X<sub>172</sub>-NSET-X<sub>177</sub>-PQK-X<sub>181</sub>-SLEE-X<sub>186</sub>-DFYKTKIKLCILLHAFRIRAVTI-  
X<sub>210</sub>-R-X<sub>212</sub>-X<sub>213</sub>-SYLN-X<sub>218</sub>-S, or a conservatively substituted variation thereof,

where X<sub>24</sub> is N or S; X<sub>27</sub> is V or T; X<sub>28</sub> is A or T; X<sub>30</sub> is P or A; X<sub>31</sub> is D, S, or G; X<sub>34</sub>  
is M or R; X<sub>35</sub> is F, S, or L; X<sub>36</sub> is P or is deleted; X<sub>39</sub> is H or D; X<sub>40</sub> is H or Y; X<sub>46</sub> is R or K;  
X<sub>48</sub> is V or A; X<sub>51</sub> is M or T; X<sub>54</sub> is K or R; X<sub>56</sub> is K or R; X<sub>58</sub> is T or I; X<sub>63</sub> is P or S; X<sub>69</sub> is I  
20 or T; X<sub>76</sub> is K or Q; X<sub>91</sub> is A or I; X<sub>92</sub> is K or T; X<sub>98</sub> is N or A; X<sub>101</sub> is E or G; X<sub>102</sub> is T or I;  
X<sub>104</sub> is F or L; X<sub>120</sub> is T; X<sub>121</sub> is T; X<sub>124</sub> is L or H; X<sub>125</sub> is S or G; X<sub>136</sub> is V or M; X<sub>140</sub> is T or  
A; X<sub>148</sub> is D or N; X<sub>161</sub> is A or T; X<sub>162</sub> is V or A; X<sub>164</sub> is D or A; X<sub>167</sub> is M or L; X<sub>172</sub> is F or  
V; X<sub>177</sub> is V or A; X<sub>181</sub> is S or P; X<sub>186</sub> is P or L; X<sub>210</sub> is D or N; X<sub>212</sub> is M; X<sub>213</sub> is M; and X<sub>218</sub>  
is S.

25 **98.** The nucleic acid of claim 97, wherein the encoded polypeptide  
comprises at its N-terminus a sequence having at least about 90% amino acid sequence  
identity to the amino acid sequence M-X<sub>2</sub>-P-X<sub>4</sub>-R-X<sub>6</sub>-LLL-X<sub>10</sub>-X<sub>11</sub>-TLVLL-X<sub>17</sub>-HLVL-X<sub>22</sub>,  
or a conservatively substituted variation thereof,

where X<sub>2</sub> is C or Y; X<sub>4</sub> is A, L or P; X<sub>6</sub> is S or G; X<sub>10</sub> is V or I; X<sub>11</sub> is A or S; X<sub>17</sub> is D or H; and X<sub>22</sub> is A or G, and optionally includes an insertion of the amino acids P-H-L between amino acid residue positions 18 and 19.

5           **99.** The nucleic acid of claim 97, wherein the encoded polypeptide has T-cell proliferative activity in the presence of a p40 polypeptide

10           **100.** The nucleic acid of claim 97, wherein the encoded polypeptide comprises an amino acid sequence selected from the group consisting of the mature polypeptide region of SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, and SEQ ID NO:35.

15           **101.** The nucleic acid of claim 97, wherein the encoded polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, and SEQ ID NO:35.

20           **102.** The nucleic acid of claim 97, comprising a polynucleotide sequence selected from the group consisting of the mature polypeptide coding region of SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, and SEQ ID NO:25.

25           **103.** The nucleic acid of claim 102, comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, and SEQ ID NO:25.

**104.** An isolated or recombinant nucleic acid comprising a polynucleotide sequence encoding a polypeptide, the encoded polypeptide comprising:

25           an amino acid sequence comprising at least 10 contiguous amino acid residues of any one of SEQ ID NOS:26-35, and

              one or more amino acid substitution at an equivalent position to that of the amino acid sequence of a p35 polypeptide identified by SEQ ID NO:36, the one or more substitution

selected from: Cys2Tyr; Ala4(Leu or Pro); Ser6Gly; Val10Ile; Ala11Ser; Asp17His;  
Ala22Gly; Asn24Ser; Val27Thr; Ala28Thr; Pro30Ala; Asp31(Ser or Gly); Met34Arg;  
Phe35(Ser or Leu); Pro36(deleted); His39Asp; His40Tyr; Arg46Lys; Val48Ala; Met51Thr;  
Lys54Arg; Thr58Ile; Pro63Ser; Ile69Thr; Lys76Gln; Lys92Thr; Asn98Ala; Glu101Gly;  
5 Thr102Ile; Phe104Leu; Leu124His; Ser125Gly; Val136Met; Thr140Ala; Asp148Asn;  
Ala161Thr; Val162Ala; Asp164Ala; Met167Leu; Phe172Val; Val177Ala; Ser181Pro;  
Pro186Leu; Asp210Asn; and insertion of one or more of 220Leu; 221Glu; 222Ser; and  
223Ser; wherein the numbering of the amino acid residues corresponds to that of SEQ ID  
NO:36.

10                   **105.** The nucleic acid of claim 104, wherein the encoded polypeptide has T-  
cell proliferative activity in the presence of a p40 polypeptide.

**106.** The nucleic acid of claim 104, wherein the encoded polypeptide  
comprises at least 150 contiguous amino acid residues of any one of SEQ ID NOS:26-35.

15                   **107.** The nucleic acid of claim 104, wherein the encoded polypeptide  
comprises at least 170 contiguous amino acid residues of any one of SEQ ID NOS:26-35.

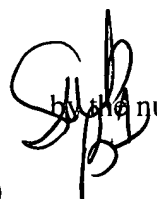
**108.** The nucleic acid of claim 104, wherein the encoded polypeptide  
comprises at least 180 contiguous amino acid residues of any one of SEQ ID NOS:26-35.

**109.** The nucleic acid of claim 104, wherein the encoded polypeptide  
comprises at least 190 contiguous amino acid residues of any one of SEQ ID NOS:26-35.

20                   **110.** An isolated or recombinant nucleic acid comprising a polynucleotide  
sequence encoding a polypeptide, the encoded polypeptide comprising at least 150  
contiguous amino acid residues of a sequence of a mature polypeptide region selected from  
the group consisting of: amino acid residues 26-221 of SEQ ID NO:26, amino acid residues  
26-221 of SEQ ID NO:27, amino acid residues 23-219 of SEQ ID NO:28, amino acid  
25 residues 23-219 of SEQ ID NO:29, amino acid residues 23-219 of SEQ ID NO:30, amino  
acid residues 23-219 of SEQ ID NO:31, amino acid residues 23-219 of SEQ ID NO:32,  
amino acid residues 23-219 of SEQ ID NO:33, amino acid residues 23-219 of SEQ ID  
NO:34, and amino acid residues 23-219 of SEQ ID NO:35.

111. The nucleic acid of claim **110**, comprising a polynucleotide sequence selected from the group consisting of: nucleotides 76 to 663 of SEQ ID NO:16; nucleotides 76 to 663 of SEQ ID NO:17; nucleotides 67 to 657 of SEQ ID NO:18; nucleotides 67 to 657 of SEQ ID NO:19, nucleotides 67 to 657 of SEQ ID NO:20; nucleotides 67 to 657 of SEQ ID NO:21; nucleotides 67 to 657 of SEQ ID NO:22; nucleotides 67 to 657 of SEQ ID NO:23; nucleotides 67 to 657 of SEQ ID NO:24; and nucleotides 67 to 657 of SEQ ID NO:25.

112. A cell comprising the nucleic acid of claim **87, 91, 97, 104, or 110.**

 113. The ~~cell~~ of claim **26**, wherein the cell expresses a polypeptide encoded by the nucleic acid.

114. A vector comprising the nucleic acid of claim **87, 91, 97, 104, or 110.**

115. The vector of claim **114**, wherein the vector comprises a plasmid, a cosmid, a phage, or a virus.

116. The vector of claim **114**, wherein the vector is an expression vector.

117. A cell transduced by the vector of claim **114.**

118. A composition comprising the nucleic acid of claim **87, 91, 97, 104, or 110** and an excipient.

119. The composition of claim **118**, wherein the excipient is a pharmaceutically acceptable excipient.

120. A composition produced by digesting one or more nucleic acids of claim **87, 91, 97, 104, or 110** with a restriction endonuclease, an RNase, or a DNase.

121. A composition produced by a process comprising incubating one or more nucleic acids of claim **87, 91, 97, 104, or 110** in the presence of deoxyribonucleotide triphosphates and a nucleic acid polymerase.

122. The composition of claim **121**, wherein the nucleic acid polymerase is a thermostable polymerase.

123. An isolated or recombinant polypeptide encoded by the nucleic acid of  
claim 87, 91, 97, 104, or 110.

124. The polypeptide of claim 123, comprising a sequence selected from the  
group consisting of: amino acid residues 26-221 of SEQ ID NO:26, amino acid residues 26-  
221 of SEQ ID NO:27, amino acid residues 23-219 of SEQ ID NO:28, amino acid residues  
23-219 of SEQ ID NO:29, amino acid residues 23-219 of SEQ ID NO:30, amino acid  
residues 23-219 of SEQ ID NO:31, amino acid residues 23-219 of SEQ ID NO:32, amino  
acid residues 23-219 of SEQ ID NO:33, amino acid residues 23-219 of SEQ ID NO:34, and  
amino acid residues 23-219 of SEQ ID NO:35.

125. The polypeptide of claim 123, comprising an N-terminal sequence  
comprising a sequence selected from the group consisting of: amino acid residues 1-25 of  
SEQ ID NOS:26 to 27, and amino acid residues 1-22 of SEQ ID NOS:28 to 35

126. The polypeptide of claim 123, having T-cell proliferative activity in the  
presence of a p40 polypeptide.

127. An isolated or recombinant modified p35 polypeptide comprising a  
modification at an equivalent position to that in the amino acid sequence of a human p35  
polypeptide (SEQ ID NO:36), the modification selected from the group consisting of:

(a) a substitution of the specified amino acid for a different amino acid at one or  
more equivalent position selected from Thr91, Met120, Ala121, Val212, Thr213, and  
Ala218;

(b) a insertion of one or more amino acid residues Phe-His-Leu between equivalent  
positions Leu19 and Ser20;

(c) a deletion of the amino acid at equivalent position Pro36

(d) at least two of (a), (b), or (c);

wherein the numbering of amino acid residue positions corresponds to that of SEQ ID  
NO:36.

128. The polypeptide of claim 127, comprising one or more substitution  
selected from the group consisting of:

Thr91(Ala or Ile); Met120Thr; Ala121Thr; Val212Met; Thr213Met; and Ala218Ser.

**129.** The polypeptide of claim **127**, comprising one or more substitution selected from the group consisting of:

Cys2Tyr; Ala4(Leu or Pro); Ser6Gly; Val10Ile; Ala11Ser; Asp17His; Ala22Gly;  
5 Asn24Ser; Val27Thr; Ala28Thr; Pro30Ala; Asp31(Ser or Gly); Met34Arg; Phe35(Ser or  
Leu); Pro36(deleted); His39Asp; His40Tyr; Arg46Lys; Val48Ala; Met51Thr; Lys54Arg;  
Thr58Ile; Pro63Ser; Ile69Thr; Lys76Gln; Lys92Thr; Asn98Ala; Glu101Gly; Thr102Ile;  
Phe104Leu; Leu124His; Ser125Gly; Val136Met; Thr140Ala; Asp148Asn; Ala161Thr;  
Val162Ala; Asp164Ala; Met167Leu; Phe172Val; Val177Ala; Ser181Pro; Pro186Leu;  
10 Asp210Asn; and insertion of one or more of 220Leu; 221Glu; 222Ser; and 223Ser.

**130.** The polypeptide of claim **127**, having T-cell proliferative activity in the presence of a p40 polypeptide.

**131.** An isolated or recombinant polypeptide, the polypeptide comprising a  
sequence having at least about 90% amino acid sequence identity to the amino acid sequence  
15 R-X<sub>24</sub>-LP-X<sub>27</sub>-X<sub>28</sub>-T-X<sub>30</sub>-X<sub>31</sub>-PG-X<sub>34</sub>-X<sub>35</sub>-X<sub>36</sub>-CL-X<sub>39</sub>-X<sub>40</sub>-SQNLL-X<sub>46</sub>-A-X<sub>48</sub>-SN-X<sub>51</sub>-LQ-  
X<sub>54</sub>-A-X<sub>56</sub>-Q-X<sub>58</sub>-LEFY-X<sub>63</sub>-CTSEE-X<sub>69</sub>-DHEDIT-X<sub>76</sub>-DKTSTVEACLPLEL-X<sub>91</sub>-X<sub>92</sub>-  
NESCL-X<sub>98</sub>-SR-X<sub>101</sub>-X<sub>102</sub>-S-X<sub>104</sub>-ITNGSCLASRKTSFM-X<sub>120</sub>-X<sub>121</sub>-LC-X<sub>124</sub>-X<sub>125</sub>-  
SIYEDLKMYQ-X<sub>136</sub>-EFK-X<sub>140</sub>-MNAKLLM-X<sub>148</sub>-PKRQIFLDQNML-X<sub>161</sub>-X<sub>162</sub>-I-X<sub>164</sub>-EL-  
X<sub>167</sub>-QALN-X<sub>172</sub>-NSET-X<sub>177</sub>-PQK-X<sub>181</sub>-SLEE-X<sub>186</sub>-DFYKTKIKLCILLHAFRIRAVTI-  
20 X<sub>210</sub>-R-X<sub>212</sub>-X<sub>213</sub>-SYLN-X<sub>218</sub>-S, or a conservatively substituted variation thereof,

where X<sub>24</sub> is N or S; X<sub>27</sub> is V or T; X<sub>28</sub> is A or T; X<sub>30</sub> is P or A; X<sub>31</sub> is D, S, or G; X<sub>34</sub>  
is M or R; X<sub>35</sub> is F, S, or L; X<sub>36</sub> is P or is deleted; X<sub>39</sub> is H or D; X<sub>40</sub> is H or Y; X<sub>46</sub> is R or K;  
X<sub>48</sub> is V or A; X<sub>51</sub> is M or T; X<sub>54</sub> is K or R; X<sub>56</sub> is K or R; X<sub>58</sub> is T or I; X<sub>63</sub> is P or S; X<sub>69</sub> is I  
or T; X<sub>76</sub> is K or Q; X<sub>91</sub> is A or I; X<sub>92</sub> is K or T; X<sub>98</sub> is N or A; X<sub>101</sub> is E or G; X<sub>102</sub> is T or I;  
25 X<sub>104</sub> is F or L; X<sub>120</sub> is T; X<sub>121</sub> is T; X<sub>124</sub> is L or H; X<sub>125</sub> is S or G; X<sub>136</sub> is V or M; X<sub>140</sub> is T or  
A; X<sub>148</sub> is D or N; X<sub>161</sub> is A or T; X<sub>162</sub> is V or A; X<sub>164</sub> is D or A; X<sub>167</sub> is M or L; X<sub>172</sub> is F or  
V; X<sub>177</sub> is V or A; X<sub>181</sub> is S or P; X<sub>186</sub> is P or L; X<sub>210</sub> is D or N; X<sub>212</sub> is M; X<sub>213</sub> is M; and X<sub>218</sub>  
is S.

**132.** The polypeptide of claim 131, having T-cell proliferative activity in the presence of a p40 polypeptide.

**133.** The polypeptide of claim 131, comprising a sequence selected from the group consisting of: amino acid residues 26-221 of SEQ ID NO:26, amino acid residues 26-221 of SEQ ID NO:27, amino acid residues 23-219 of SEQ ID NO:28, amino acid residues 23-219 of SEQ ID NO:29, amino acid residues 23-219 of SEQ ID NO:30, amino acid residues 23-219 of SEQ ID NO:31, amino acid residues 23-219 of SEQ ID NO:32, amino acid residues 23-219 of SEQ ID NO:33, amino acid residues 23-219 of SEQ ID NO:34, and amino acid residues 23-219 of SEQ ID NO:35.

**134.** A polypeptide comprising at least 100 contiguous amino acid residues of a protein encoded by a coding polynucleotide sequence, the polynucleotide sequence selected from the group consisting of:

(a) nucleotides 76 to 663 of SEQ ID NO:16, nucleotides 76 to 663 of SEQ ID NO:17, nucleotides 67 to 657 of SEQ ID NO:18, nucleotides 67 to 657 of SEQ ID NO:19, nucleotides 67 to 657 of SEQ ID NO:20, nucleotides 67 to 657 of SEQ ID NO:21, nucleotides 67 to 657 of SEQ ID NO:22, nucleotides 67 to 657 of SEQ ID NO:23, nucleotides 67 to 657 of SEQ ID NO:24, and nucleotides 67 to 657 of SEQ ID NO:25;

(b) a coding polynucleotide sequence that encodes a first polypeptide selected from amino acid residues 26-221 of SEQ ID NO:26, amino acid residues 26-221 of SEQ ID NO:27, amino acid residues 23-219 of SEQ ID NO:28, amino acid residues 23-219 of SEQ ID NO:29, amino acid residues 23-219 of SEQ ID NO:30, amino acid residues 23-219 of SEQ ID NO:31, amino acid residues 23-219 of SEQ ID NO:32, amino acid residues 23-219 of SEQ ID NO:33, amino acid residues 23-219 of SEQ ID NO:34, and amino acid residues 23-219 of SEQ ID NO:35; and

(c) a complementary polynucleotide sequence which hybridizes under highly stringent conditions over substantially an entire length of a polynucleotide sequence of (a) or (b).

**135.** The polypeptide of claim 134, comprising at least 150 contiguous amino acid residues of the encoded protein.

136. The polypeptide of claim 134, comprising a sequence selected from the group consisting of the mature polypeptide region of SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, and SEQ ID NO:35.

5 137. The polypeptide of claim 134, comprising a sequence selected from the group consisting of SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, and SEQ ID NO:35.

10 138. The polypeptide of claim 134, having T-cell proliferative activity in the presence of a p40 polypeptide.

139. The polypeptide of claim 127, 131, or 134, comprising a secretion/localization sequence or a polypeptide subsequence that facilitates purification.

15 140. The polypeptide of claim 139, wherein the subsequence that facilitates purification is selected from the group consisting of: an epitope tag, a polyhistidine tag, and a GST fusion.

141. The polypeptide of claim 127, 131, or 134, comprising a Met at the N-terminus.

142. The polypeptide of claim 127, 131, or 134, comprising a modified amino acid.

20 143. The polypeptide of claim 142, wherein the modified amino acid is selected from the group consisting of: a glycosylated amino acid, a PEGylated amino acid, a farnesylated amino acid, an acetylated amino acid, and a biotinylated amino acid.

144. A composition comprising the polypeptide of claim 127, 131, or 134.

145. The composition of claim 144, further comprising a p40 polypeptide.

25 146. The composition of claim 144, further comprising an excipient.



**147.** The composition of claim **146**, wherein the excipient is a pharmaceutically acceptable excipient.

**148.** A polypeptide which is specifically bound by a polyclonal antisera raised against at least one antigen, said at least one antigen comprising at least one amino acid sequence of SEQ ID NO:26 to SEQ ID NO:35, or a fragment thereof, wherein the antisera is subtracted with a p35 polypeptide encoded by a nucleic acid corresponding to one or more of GenBank accession number: M65271, M65291, U19842, U19835, U83185, Y07761, AF054605, U49085, L35765, Y11130, U14416, U57751, AF173557, AF003542, X97018, AF177031, M86672, and S82419.

**149.** An antibody or antisera produced by administering the polypeptide of claim **127**, **131**, or **134** to a mammal, which antibody specifically binds at least one antigen, said at least one antigen comprising a polypeptide comprising one or more of the amino acid sequences of SEQ ID NO:26 to SEQ ID NO:35, which antibody or antisera does not specifically bind to a p35 polypeptide encoded by a nucleic acid corresponding to one or more of GenBank accession number: M65271, M65291, U19842, U19835, U83185, Y07761, AF054605, U49085, L35765, Y11130, U14416, U57751, AF173557, AF003542, X97018, AF177031, M86672, and S82419.

**150.** An antibody or antisera which specifically binds a polypeptide, the polypeptide comprising a sequence selected from the group consisting of SEQ ID NO:26 to SEQ ID NO:35, wherein the antibody does not specifically bind to a p35 polypeptide encoded by a nucleic acid corresponding to one or more of GenBank accession number: M65271, M65291, U19842, U19835, U83185, Y07761, AF054605, U49085, L35765, Y11130, U14416, U57751, AF173557, AF003542, X97018, AF177031, M86672, and S82419.

**151.** A method of producing a polypeptide, the method comprising:  
introducing into a population of cells a nucleic acid of claim **87**, **91**, **97**, **104**, or **110**, the nucleic acid operatively linked to a regulatory sequence effective to produce the encoded polypeptide; and  
culturing the cells in a culture medium to produce the polypeptide.

152. A method of producing a polypeptide, the method comprising  
introducing into a population of cells a recombinant expression vector comprising the  
nucleic acid of claim 87, 91, 97, 104, or 110; and  
culturing the cells in a culture medium under conditions suitable to produce the  
5 polypeptide encoded by the expression vector.

153. A method of inducing proliferation of T-lymphocytes, the method  
comprising: contacting the T-lymphocytes with a composition of claim 144, thereby inducing  
proliferation of the T-lymphocytes.

154. The method of claim 153, wherein the T-lymphocytes are in culture.

10 155. A method of inducing production of IFN- $\gamma$  in T-lymphocytes, the method  
comprising:  
contacting the T-lymphocytes with a composition of claim 144, thereby inducing  
production of IFN- $\gamma$  in the T-lymphocytes.

156. The method of claim 155, wherein the T-lymphocytes are in culture.

15 157. A method for making a modified or recombinant nucleic acid, the  
method comprising: recursively recombining one or more nucleic acids of claim 87, 91, 97,  
104, or 110 with one or more additional nucleic acid, the additional nucleic acid encoding a  
p35 polypeptide or subsequence thereof.

20 158. The method of claim 157, wherein said recursive recombination  
produces at least one library of recombinant modified p35 nucleic acids.

159. A nucleic acid library produced by the method of claim 158.

160. A population of cells comprising the library of claim 159.

161. A recombinant modified p35 nucleic acid produced by the method of  
claim 157.

25 162. A cell comprising the nucleic acid of claim 161.

163. The method of claim 157, wherein the recursive recombination is performed *in vitro*.

164. The method of claim 157, wherein the recursive recombination is performed *in vivo* or *ex vivo*..

5 165. A composition comprising two or more nucleic acids of claim 87, 91, 97, 104, or 110.

166. The composition of claim 165, wherein the composition comprises a library comprising at least ten nucleic acids.

10 167. A method of producing a modified p35 nucleic acid comprising mutating a nucleic acid of claim 87, 91, 97, 104, or 110.

168. The modified p35 nucleic acid produced by the method of claim 167.

15 169. A nucleic acid which comprises a unique subsequence in a nucleic acid selected from SEQ ID NO:16 to SEQ ID NO:25, wherein the unique subsequence is unique as compared to a nucleic acid sequence of a known p35 nucleic acid sequence or a nucleic acid corresponding to any of GenBank accession number: M65271, M65291, U19842, U19835, U83185, Y07761, AF054605, U49085, L35765, Y11130, U14416, U57751, AF173557, AF003542, X97018, AF177031, M86672, and S82419.

20 170. A polypeptide which comprises a unique subsequence in a polypeptide selected from: SEQ ID NO:26 to SEQ ID NO:35, wherein the unique subsequence is unique as compared to a sequence of a known p35 polypeptide or a sequence of a polypeptide encoded by a nucleic acid corresponding to any of GenBank accession number: M65271, M65291, U19842, U19835, U83185, Y07761, AF054605, U49085, L35765, Y11130, U14416, U57751, AF173557, AF003542, X97018, AF177031, M86672, and S82419.

25 171. A target nucleic acid which hybridizes under stringent conditions to a unique coding oligonucleotide which encodes a unique subsequence in a polypeptide selected from: SEQ ID NO:26 to SEQ ID NO:35, wherein the unique subsequence is unique as compared to a sequence of a known p35 polypeptide or a sequence of a polypeptide encoded

by a nucleic acid corresponding to any of GenBank accession number: M65271, M65291, U19842, U19835, U83185, Y07761, AF054605, U49085, L35765, Y11130, U14416, U57751, AF173557, AF003542, X97018, AF177031, M86672, and S82419.

5        **172.** The nucleic acid of claim **171**, wherein the stringent conditions are selected such that a perfectly complementary oligonucleotide to the unique coding oligonucleotide hybridizes to the unique coding oligonucleotide with at least a 5x higher signal to noise ratio than for hybridization of the perfectly complementary oligonucleotide to a control nucleic acid corresponding to any of GenBank accession number: M65271, M65291, U19842, U19835, U83185, Y07761, AF054605, U49085, L35765, Y11130, 10        U14416, U57751, AF173557, AF003542, X97018, AF177031, M86672, and S82419, wherein the target nucleic acid hybridizes to the unique coding oligonucleotide with at least a 2x higher signal to noise ratio as compared to hybridization of the control nucleic acid to the coding oligonucleotide.

15        **173.** A computer or computer readable medium comprising a database comprising a sequence record comprising one or more character string corresponding to a nucleic acid or protein sequence selected from SEQ ID NO:1 to SEQ ID NO:14, SEQ ID NO:16 to SEQ ID NO:35, SEQ ID NO:39, and SEQ ID NO:40.

20        **174.** An integrated system comprising a computer or computer readable medium comprising a database comprising one or more sequence records, each comprising one or more character strings corresponding to a nucleic acid or protein sequence selected from SEQ ID NO:1 to SEQ ID NO:14, SEQ ID NO:16 to SEQ ID NO:35, SEQ ID NO:39, and SEQ ID NO:40, the integrated system further comprising a user input interface allowing a user to selectively view one or more sequence record.

25        **175.** The integrated system of claim **174**, the computer or computer readable medium comprising an alignment instruction set which aligns the character strings with one or more additional character string corresponding to a nucleic acid or protein sequence.

176. The integrated system of claim 175, wherein the instruction set comprises one or more of: a local homology comparison determination, a homology alignment determination, a search for similarity determination, and a BLAST determination.

5 177. The integrated system of claim 175, further comprising a user readable output element which displays an alignment produced by the alignment instruction set.

178. The integrated system of claim 174, the computer or computer readable medium further comprising an instruction set which translates one or more nucleic acid sequence comprising a sequence selected from SEQ ID NO:1 to SEQ ID NO:7 and SEQ ID NO:16 to SEQ ID NO:25, into an amino acid sequence.

10 179. The integrated system of claim 174, the computer or computer readable medium further comprising an instruction set for reverse-translating one or more amino acid sequence comprising a sequence selected from SEQ ID NO:8 to SEQ ID NO:14, SEQ ID NO:26 to SEQ ID NO:35, SEQ ID NO:39, and SEQ ID NO:40 into a nucleic acid sequence.

15 180. The integrated system of claim 179, wherein the instruction set selects the nucleic acid sequence by applying a codon usage instruction set or an instruction set which determines sequence identity to a test nucleic acid sequence.

20 181. A method of using a computer system to present information pertaining to at least one of a plurality of sequence records stored in a database, said sequence records each comprising one or more character string corresponding to SEQ ID NO:1 to SEQ ID NO:14, SEQ ID NO:16 to SEQ ID NO:35, SEQ ID NO:39, and SEQ ID NO:40, the method comprising:

determining a list of one or more character strings corresponding to one or more of SEQ ID NO:1 to SEQ ID NO:14, SEQ ID NO:16 to SEQ ID NO:35, SEQ ID NO:39, and SEQ ID NO:40 or a subsequence thereof;

25 determining which character strings of said list are selected by a user; and

displaying the selected character strings, or aligning the selected character strings with an additional character string.

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